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RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/894,657   TIME: 12:56:28

Input Set : **N:\Crf3\RULE60\09894657.txt**
Output Set: **N:\CRF3\12072001\I894657.raw**

SEQUENCE LISTING
C--> 3 (1) **GENERAL INFORMATION:**
5   (i) APPLICANT: Hillman, Jennifer L.
6   Yue, Henry
7   Lal, Preeti
8   Shah, Purvi
9   Corley, Neil C.
C--> 11   (ii) **TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL**
12   **PROLIFERATION**
14   (iii) NUMBER OF SEQUENCES: 9
16   (iv) CORRESPONDENCE ADDRESS:
17   (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
18   (B) STREET: 3174 Porter Dr.
19   (C) CITY: Palo Alto
20   (D) STATE: CA
21   (E) COUNTRY: USA
22   (F) ZIP: 94304
24   (v) COMPUTER READABLE FORM:
25   (A) MEDIUM TYPE: Diskette
26   (B) COMPUTER: IBM Compatible
27   (C) OPERATING SYSTEM: DOS
28   (D) SOFTWARE: FastSEQ for Windows Version 2.0
30   (vi) CURRENT APPLICATION DATA:
C--> 31   (A) **APPLICATION NUMBER: US/09/894,657**
C--> 32   (B) **FILING DATE: 28-Jun-2001**
34   (vii) PRIOR APPLICATION DATA:
35   (A) APPLICATION NUMBER: 09/410,372
36   (B) FILING DATE:
39   (viii) ATTORNEY/AGENT INFORMATION:
40   (A) NAME: Billings, Lucy J.
41   (B) REGISTRATION NUMBER: 36,749
42   (C) REFERENCE/DOCKET NUMBER: PF-0421 US
44   (ix) TELECOMMUNICATION INFORMATION:
45   (A) TELEPHONE: 650-855-0555
46   (B) TELEFAX: 650-845-4166
49 (2) INFORMATION FOR SEQ ID NO: 1:
51   (i) SEQUENCE CHARACTERISTICS:
52   (A) LENGTH: 168 amino acids
53   (B) TYPE: amino acid
54   (C) STRANDEDNESS: single
55   (D) TOPOLOGY: linear
57   (vii) IMMEDIATE SOURCE:
58   (A) LIBRARY: SYNORAB01
59   (B) CLONE: 358673
61   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63   Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
64   1   5   10   15

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65	Ser	Ala	Glu	Arg	Gly	Leu	Gly	Pro	Ser	Pro	Ala	Gly	Asp	Gly	Pro	Ser
66			20					25				30			

```
65   Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
66           20              25              30
67   Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
68           35              40              45
69·  Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
70        50              55              60
71   Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
72   65              70              75              80
73   Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
74              85              90              95
75   Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
76           100             105             110
77   Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
78           115             120             125
79   Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
80        130             135             140
81   Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
82   145             150             155             160
83   Arg Gly Ser Ser Ala Pro Ser Gln
84                   165
```

86   (2) INFORMATION FOR SEQ ID NO: 2:
88   (i) SEQUENCE CHARACTERISTICS:
89   (A) LENGTH: 1105 base pairs
90   (B) TYPE: nucleic acid
91   (C) STRANDEDNESS: single
92   (D) TOPOLOGY: linear
94   (vii) IMMEDIATE SOURCE:
95   (A) LIBRARY: 358673
96   (B) CLONE: SYNORAB01
98   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
100  CGACCGTCCG CGGGAGACTG AGGTCCTGAG CCGACAGCCT CAGCTCCCTG CCAGGCCAGA    60
101  CCCGGCAGAC AGATGAGGGC CCAGGAGGCC TGGCGGGCCT GGGGGCGCTA CGGTGGGAGA   120
102  GGAAGCCAGG GGTACCTGCC TCTGCCTTCC AGGGCCACCG TTGGCCCCAG CTGTGCCTTG   180
103  ACTACGTAAC ATCTTGTCCT CACAGCCCAG AGCATGTTCC AGATCCCAGA GTTTGAGCCG   240
104  AGTGAGCAGG AAGACTCCAG CTCTGCAGAG AGGGGCCTGG GCCCCAGCCC CGCAGGGGAC   300
105  GGGCCCTCAG GCTCCGGCAA GCATCATCGC CAGGCCCCAG GCCTCCTGTG GACGCCAGT    360
106  CACCAGCAGG AGCAGCCAAC CAGCAGCAGC CATCATGGAG GCGCTGGGGC TGTGGAGATC   420
107  CGGAGTCGCC ACAGCTCCTA CCCCGCGGGG ACGGAGGACG ACGAAGGGAT GGGGGAGGAG   480
108  CCCAGCCCCT TTCGGGGCCG CTCGCGCTCG GCGCCCCCCA ACCTCTGGGC AGCACAGCGC   540
109  TATGGCCGCG AGCTCCGGAG GATGAGTGAC GAGTTTGTGG ACTCCTTTAA GAAGGGACTT   600
110  CCTCGCCCGA AGAGCGCGGG CACAGCAACG CAGATGCGGC AAAGCTCCAG CTGGACGCGA   660
111  GTCTTCCAGT CCTGGTGGGA TCGGAACTTG GGCAGGGGAA GCTCCGCCCC CTCCCAGTGA   720
112  CCTTCGCTCC ACATCCCGAA ACTCCACCCG TTCCCACTGC CCTGGGCAGC CATCTTGAAT   780
113  ATGGGCGGAA GTACTTCCCT CAGGCCTATG CAAAAAGAGG ATCCGTGCTG TCTCCTTTGG   840
114  AGGGAGGGCT GACCCAGATT CCCTTCCGGT GCGTGTGAAG CCACGGAAGG CTTGGTCCCA   900
115  TCGGAAGTTT TGGGTTTTCC GCCCACAGCC GCCGGAAGTG GCTCCGTGGC CCCGCCCTCA   960
116  GGCTCCGGGC TTTCCCCCAG GCGCCTGCGC TAAGTCGCGA GCCAGGTTTA ACCGTTGCGT  1020
117  CACCGGGACC CGAGCCCCCG CGATGCCCTG GGGGCCGTGC TCACTACCAA ATGTTAATAA  1080
118  AGCCCGCGTC TGTGCAAAAA AAAAA                                        1105
```

RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/894,657   TIME: 12:56:28

Input Set : N:\Crf3\RULE60\09894657.txt
Output Set: N:\CRF3\12072001\I894657.raw

```
120 (2) INFORMATION FOR SEQ ID NO: 3:
122       (i) SEQUENCE CHARACTERISTICS:
123            (A) LENGTH: 440 amino acids
124            (B) TYPE: amino acid
125            (C) STRANDEDNESS: single
126            (D) TOPOLOGY: linear
128      (vii) IMMEDIATE SOURCE:
129            (A) LIBRARY: LATRTUT02
130            (B) CLONE: 1352286
132      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
134  Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala
135   1               5                  10                  15
136  Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His
137            20                  25                  30
138  Gly Arg Ala Gly Gly Gly Arg Arg Gly Ser Asn Pro Val Lys Arg Tyr
139            35                  40                  45
140  Ala Pro Gly Leu Pro Cys Asp Val Tyr Thr Tyr Leu His Glu Lys Tyr
141        50                  55                  60
142  Leu Asp Cys Gln Glu Arg Lys Leu Val Tyr Val Leu Pro Gly Trp Pro
143  65                  70                  75                  80
144  Gln Asp Leu Leu His Met Leu Leu Ala Arg Asn Lys Ile Arg Thr Leu
145                85                  90                  95
146  Lys Asn Asn Met Phe Ser Lys Phe Lys Lys Leu Lys Ser Leu Asp Leu
147            100                 105                 110
148  Gln Gln Asn Glu Ile Ser Lys Ile Glu Ser Glu Ala Phe Phe Gly Leu
149            115                 120                 125
150  Asn Lys Leu Thr Thr Leu Leu Leu Gln His Asn Gln Ile Lys Val Leu
151        130                 135                 140
152  Thr Glu Glu Val Phe Ile Tyr Thr Pro Leu Leu Ser Tyr Leu Arg Leu
153  145                 150                 155                 160
154  Tyr Asp Asn Pro Trp His Cys Thr Cys Glu Ile Glu Thr Leu Ile Ser
155            165                 170                 175
156  Met Leu Gln Ile Pro Arg Asn Arg Asn Leu Gly Asn Tyr Ala Lys Cys
157            180                 185                 190
158  Glu Ser Pro Gln Glu Gln Lys Asn Lys Lys Leu Arg Gln Ile Lys Ser
159            195                 200                 205
160  Glu Gln Leu Cys Asn Glu Glu Lys Glu Gln Leu Asp Pro Lys Pro Gln
161        210                 215                 220
162  Val Ser Gly Arg Pro Pro Val Ile Lys Pro Glu Val Asp Ser Thr Phe
163  225                 230                 235                 240
164  Cys His Asn Tyr Val Phe Pro Ile Gln Thr Leu Asp Cys Lys Arg Lys
165            245                 250                 255
166  Glu Leu Lys Lys Val Pro Asn Asn Ile Pro Pro Asp Ile Val Lys Leu
167            260                 265                 270
168  Asp Leu Ser Tyr Asn Lys Ile Asn Gln Leu Arg Pro Lys Glu Phe Glu
169            275                 280                 285
170  Asp Val His Glu Leu Lys Lys Leu Asn Leu Ser Ser Asn Gly Ile Glu
171        290                 295                 300
172  Phe Ile Asp Pro Ala Ala Phe Leu Gly Leu Thr His Leu Glu Glu Leu
```

RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/894,657   TIME: 12:56:28

Input Set : N:\Crf3\RULE60\09894657.txt
Output Set: N:\CRF3\12072001\I894657.raw

```
173  305                    310                  315                    320
174  Asp Leu Ser Asn Asn Ser Leu Gln Asn Phe Asp Tyr Gly Val Leu Glu
175              325                  330                    335
176  Asp Leu Tyr Phe Leu Lys Leu Leu Trp Leu Arg Asp Asn Pro Trp Arg
177          340                    345                  350
178  Cys Asp Tyr Asn Ile His Tyr Leu Tyr Tyr Trp Leu Lys His His Tyr
179          355                  360                  365
180  Asn Val His Phe Asn Gly Leu Glu Cys Lys Thr Pro Glu Glu Tyr Lys
181      370                  375                  380
182  Gly Trp Ser Val Gly Lys Tyr Ile Arg Ser Tyr Tyr Glu Glu Cys Pro
183  385                  390                  395                    400
184  Lys Asp Lys Leu Pro Ala Tyr Pro Glu Ser Phe Asp Gln Asp Thr Glu
185              405                  410                  415
186  Asp Asp Glu Trp Glu Lys Lys His Arg Asp His Thr Ala Lys Lys Gln
187          420                  425                  430
188  Ser Val Ile Ile Thr Ile Val Gly
189          435                  440
191  (2) INFORMATION FOR SEQ ID NO: 4:
193       (i)  SEQUENCE CHARACTERISTICS:
194            (A)  LENGTH: 2082 base pairs
195            (B)  TYPE: nucleic acid
196            (C)  STRANDEDNESS: single
197            (D)  TOPOLOGY: linear
199      (vii) IMMEDIATE SOURCE:
200            (A)  LIBRARY: LATRTUT02
201            (B)  CLONE: 1352286
203      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
205  GAATGCAGCC CATTCTCTGG AGAACTTCCT CACACACCGC AGCAAAGAGA AGACTGAAAG      60
206  ACAAACCTGG GTGCAGCCAG AGAGGTCCAG ATAGATGAGC TTGTGGCATC CATTCCCCAA     120
207  GTTCAGCCTA GGGACTCCAC GTACCCCAGC TGGGTCTCAT TGTTCCAGAA CTGCATTAGT     180
208  TAAGATTACC CAGACTTGGA TTTCAAAGGA ATACTTTCAT TGTTCCGTCT GTAACACGAA     240
209  GTAATTGGGG CCAGCTGGAT GTCAGGATGC GTGTGGTTAC CATTGTAATC TTGCTCTGCT     300
210  TTTGCAAAGC GGCTGAGCTG CGCAAAGCAA GCCCAGGCAG TGTGAGAAGC CGAGTGAATC     360
211  ATGGCCGGGC GGGTGGAGGC CGGAGAGGCT CCAACCCGGT CAAACGCTAC GCACCAGGCC     420
212  TCCCGTGTGA CGTGTACACA TATCTCCATG AGAAATACTT AGATTGTCAA GAAAGAAAAT     480
213  TAGTTTATGT GCTGCCTGGT TGGCCTCAGG ATTTGCTGCA CATGCTGCTA GCAAGAAACA     540
214  AGATCCGCAC ATTGAAGAAC AACATGTTTT CCAAGTTTAA AAAGCTGAAA AGCCTGGATC     600
215  TGCAGCAGAA TGAGATCTCT AAAATTGAGA GTGAGGCGTT CTTTGGTTTA AACAAACTCA     660
216  CCACCCTCTT ACTGCAGCAC AACCAGATCA AAGTCTTGAC GGAGGAAGTG TTCATTTACA     720
217  CACCTCTCTT GAGCTACCTG CGTCTTTATG ACAACCCCTG GCACTGTACT TGTGAGATAG     780
218  AAACGCTTAT TTCAATGTTG CAGATTCCCA GGAACCGGAA TTTGGGGAAC TACGCCAAGT     840
219  GTGAAAGTCC ACAAGAACAA AAAATAAAA AACTGCGGCA GATAAAATCT GAACAGTTGT     900
220  GTAATGAAGA AAAGGAACAA TTGGACCCGA AACCCCAAGT GTCAGGGAGA CCCCCAGTCA     960
221  TCAAGCCTGA GGTGGACTCA ACTTTTTGCC ACAATTATGT GTTTCCCATA CAAACACTGG    1020
222  ACTGCAAAAG GAAAGAGTTG AAAAAAGTGC CAAACAACAT CCCTCCAGAT ATTGTTAAAC    1080
223  TTGACTTGTC ATACAATAAA ATCAACCAAC TTCGACCCAA GGAATTTGAA GATGTTCATG    1140
224  AGCTGAAGAA ATTAAACCTC AGCAGCAATG GCATTGAATT CATCGATCCT GCCGCTTTTT    1200
225  TAGGGCTCAC ACATTTAGAA GAATTAGATT TATCAAACAA CAGTCTGCAA AACTTTGACT    1260
226  ATGGCGTATT AGAAGACTTG TATTTTTTGA AACTCTTGTG GCTCAGAGAT AACCCTTGGA    1320
```

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227  GATGTGACTA CAACATTCAC TACCTCTACT ACTGGTTAAA GCACCACTAC AATGTCCATT  1380
228  TTAATGGCCT GGAATGCAAA ACGCCTGAAG AATACAAAGG ATGGTCTGTG GGAAAATATA  1440
229  TTAGAAGTTA CTATGAAGAA TGCCCCAAAG ACAAGTTACC AGCATATCCT GAGTCATTTG  1500
230  ACCAAGACAC AGAAGATGAT GAATGGGAAA AAAAACATAG AGATCACACC GCAAAGAAGC  1560
231  AAAGCGTAAT AATTACTATA GTAGGATAAG GTAGAAATTG TTCTGATTGT AATTAGTTTT  1620
232  GTATTTTCTA TACTGGTGTT AGAAAACATA TGTTTACATT TGATTAACTG TGTTGCCTAT  1680
233  TTATGCAGGG TAATCCAGCT AAAGGAAGCT TTCTTTAATT ATAAGTATTA TTGTGACTAT  1740
234  TATAGTAATC AAGAGAATGC TATCATCCTG CTTGCCTGTC CATTTGTGGA ACAGCATCTG  1800
235  GTGATATGCA ATTCCACACT GGTAACCTGC AGCAGTTGGG TCCTAATGAT GGCATTAGAC  1860
236  TTTCATAATG TCCTGTATAA ATGTTTTTAC TGCTTTTAGA AAATAAAGAA AAAAAACTTG  1920
237  GTTCATGTTT ACATGCCTTT CGATAGCTGT TTGTGCATAC TTAAAGATGA TCAAAATGAT  1980
238  TTTATACAAA TGCTGTTATA ATAAAATGTC ATTCCCTACC CCTCTACTTT TTTTCAGTAA  2040
239  GTCATCTTAT ACATTAAATA AATTTCCATT TCTGAAAAAA AA                      2082
```

241 (2) INFORMATION FOR SEQ ID NO: 5:
243   (i) SEQUENCE CHARACTERISTICS:
244   (A) LENGTH: 469 amino acids
245   (B) TYPE: amino acid
246   (C) STRANDEDNESS: single
247   (D) TOPOLOGY: linear
249   (vii) IMMEDIATE SOURCE:
250   (A) LIBRARY: OVARTUT01
251   (B) CLONE: 815087
253   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
255 Met Asp Val Glu Asn Glu Gln Ile Leu Asn Val Asn Pro Ala Asp Pro
256 1   5   10   15
257 Asp Asn Leu Ser Asp Ser Leu Phe Ser Gly Asp Glu Glu Asn Ala Gly
258   20   25   30
259 Thr Glu Glu Val Lys Asn Glu Ile Asn Gly Asn Trp Ile Ser Ala Ser
260   35   40   45
261 Ser Ile Asn Glu Ala Arg Ile Asn Ala Lys Ala Lys Arg Arg Leu Arg
262   50   55   60
263 Lys Asn Ser Ser Arg Asp Ser Gly Arg Gly Asp Ser Val Ser Asp Ser
264 65   70   75   80
265 Gly Ser Asp Ala Leu Arg Ser Gly Leu Thr Val Pro Thr Ser Pro Lys
266   85   90   95
267 Gly Arg Leu Leu Asp Arg Arg Ser Arg Ser Gly Lys Gly Arg Gly Leu
268   100   105   110
269 Pro Lys Lys Gly Gly Ala Gly Gly Lys Gly Val Trp Gly Thr Pro Gly
270   115   120   125
271 Gln Val Tyr Asp Val Glu Glu Val Asp Val Lys Asp Pro Asn Tyr Asp
272   130   135   140
273 Asp Asp Gln Glu Asn Cys Val Tyr Glu Thr Val Val Leu Pro Leu Asp
274 145   150   155   160
275 Glu Arg Ala Phe Glu Lys Thr Leu Thr Pro Ile Ile Gln Glu Tyr Phe
276   165   170   175
277 Glu His Gly Asp Thr Asn Glu Val Ala Glu Met Leu Arg Asp Leu Asn
278   180   185   190
279 Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu Ala Val Ser Leu Ala
280   195   200   205

VERIFICATION SUMMARY   DATE: 12/07/2001
PATENT APPLICATION: **US/09/894,657**   TIME: 12:56:29

Input Set : **N:\Crf3\RULE60\09894657.txt**
Output Set: **N:\CRF3\12072001\I894657.raw**

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]